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[illegible]

Query Match: 46 29; Score: 651.6; pos: 2; Length: 1430;
 Best Local Similarity: 66.58; Pred. No.: 1.5e+000;
 Matches: 950; Conservation: 274; Missmatches: 225; Indels: 28; Gaps: 12

Index

SHILLINGS
STRIKES

1

	Query Match	26.6%	Score	483.2	DB	13	Length	755
	Best Local Similarity	75.6%	Pred. No.	4	30	85		
	Hatches	543	Conservation	0	3	4	149	7
Qy	583	ctadaagatggaagagaggtattatgaattcccaatgataaagttgaatactatgaatattatga	642					
Dh	722	CTGAAGTACGTTACGGCAGAGGGAAATTCGCTGAAGGGTGAATTCGTAACATGCTG	663					
Qy	643	gaagaaacacccagatgacgaagagcgcgcacacacacacacacacacacacacacacacac	702					
Dh	662	AAAGAACACCAACGGCGAAATACATCTCTGTCGGCGGACACTGACACTGACACACG	603					
Qy	703	gtatgtatgaacacagatatatataaacctgattagtcacacattatataacacattatata	762					

Sequence version 4.1
Copyright (c) 1995 Zymo Corporation Ltd.

Maximum score 99.4, using SW model

February 26, 2002, 05:24:43 Search time 7106.49 seconds

(without alignments)

334,784 hits in total

Sequence: 58599026002

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. It is derived by analysis of the total score distribution.

SUMMARY

1

Result No.	Score	Query Match	Length	Id	Accession
1	1298.4	90.4	1476	1	AF127411
2	1296.8	90.3	1476	1	AF127412
3	1295.2	90.2	1476	1	AF127413
4	1294.4	90.0	1476	1	AF127414
5	1278	89.0	1476	1	AF127415
6	1277.6	89.0	1476	1	AF127416
7	1274.8	88.7	1476	1	AF127417
8	1272.8	88.6	1476	1	AF127418
9	1266.4	87.5	1476	1	AF127419
10	1264.4	87.3	1476	1	AF127420
11	1254.4	87.3	1476	1	AF127421
12	1251.2	87.1	1476	1	AF127422
13	1250.6	87.1	1476	1	AF127423
14	1248.6	86.9	1476	1	AF127424
15	1245.8	86.8	1476	1	AF127425
16	1244.8	86.7	1476	1	AF127426
17	1241	86.4	1476	1	AF127427
18	1236.2	86.1	1476	1	AF127428
19	1234.6	86.1	1476	1	AF127429
20	1234.2	85.9	1476	1	AF127430
21	1233.4	85.9	1476	1	AF127431
22	1232.8	85.8	1476	1	AF127432
23	1232.8	85.8	1476	1	AF127433
24	1232.2	85.8	1476	1	AF127434
25	1231.8	85.8	1476	1	AF127435
26	1231.6	85.8	1476	1	AF127436
27	1230.6	85.7	1476	1	AF127437
28	1229	85.6	1476	1	AF127438
29	1228.8	85.6	1476	1	AF127439
30	1228.6	85.6	1476	1	AF127440
31	1227.8	85.5	1476	1	AF127441
32	1227.2	85.5	1476	1	AF127442
33	1227	85.4	1476	1	AF127443
34	1226.6	85.4	1476	1	AF127444
35	1226.2	85.4	1476	1	AF127445
36	1224.6	85.3	1476	1	AF127446
37	1224.6	85.3	1476	1	AF127447
38	1219	84.9	1476	1	AF127448
39	1215	84.6	1476	1	AF127449
40	1214.6	84.6	1476	1	AF127450
41	1211.4	84.4	1476	1	AF127451
42	1211	84.3	1476	1	AF127452
43	1210	84.3	1476	1	AF127453
44	1208.6	84.2	1476	1	AF127454
45	1208.2	84.1	1476	1	AF127455

ALIGNMENTS

Result No.	Score	Query Match	Length	Id	Accession
1	1298.4	90.4	1476	1	AF127411
2	1296.8	90.3	1476	1	AF127412
3	1295.2	90.2	1476	1	AF127413
4	1294.4	90.0	1476	1	AF127414
5	1278	89.0	1476	1	AF127415
6	1277.6	89.0	1476	1	AF127416
7	1274.8	88.7	1476	1	AF127417
8	1272.8	88.6	1476	1	AF127418
9	1266.4	87.5	1476	1	AF127419
10	1264.4	87.3	1476	1	AF127420
11	1254.4	87.3	1476	1	AF127421
12	1251.2	87.1	1476	1	AF127422
13	1250.6	87.1	1476	1	AF127423
14	1248.6	86.9	1476	1	AF127424
15	1245.8	86.8	1476	1	AF127425
16	1244.8	86.7	1476	1	AF127426
17	1241	86.4	1476	1	AF127427
18	1236.2	86.1	1476	1	AF127428
19	1234.6	86.1	1476	1	AF127429
20	1234.2	85.9	1476	1	AF127430
21	1233.4	85.9	1476	1	AF127431
22	1232.8	85.8	1476	1	AF127432
23	1232.8	85.8	1476	1	AF127433
24	1232.2	85.8	1476	1	AF127434
25	1231.8	85.8	1476	1	AF127435
26	1231.6	85.8	1476	1	AF127436
27	1230.6	85.7	1476	1	AF127437
28	1229	85.6	1476	1	AF127438
29	1228.8	85.6	1476	1	AF127439
30	1228.6	85.6	1476	1	AF127440
31	1227.8	85.5	1476	1	AF127441
32	1227.2	85.5	1476	1	AF127442
33	1227	85.4	1476	1	AF127443
34	1226.6	85.4	1476	1	AF127444
35	1226.2	85.4	1476	1	AF127445
36	1224.6	85.3	1476	1	AF127446
37	1224.6	85.3	1476	1	AF127447
38	1219	84.9	1476	1	AF127448
39	1215	84.6	1476	1	AF127449
40	1214.6	84.6	1476	1	AF127450
41	1211.4	84.4	1476	1	AF127451
42	1211	84.3	1476	1	AF127452
43	1210	84.3	1476	1	AF127453
44	1208.6	84.2	1476	1	AF127454
45	1208.2	84.1	1476	1	AF127455

SUMMARY

1

FEATURES		SWITZERLAND		Location/Qualifiers	
SOURCE		1. 1476		/organism "Glucobacter asaii"	
		/strain "IFO 3275"		/db_xref "taxon:38306"	
		/submitter "T. Inoue"			
rRNA		1. 1476		/product "16S ribosomal RNA"	
BASE COUNT		351 a		483 c	
ORIGIN					
Query Match		90.2%		Score: 1295.2; DB 1; Length: 1476;	
Best local Similarity		91.5%		Pred. No.: 2376; 10;	
Matches: 1348;		Conservative: 0;		Mismatches: 88;	
				Indels: 0;	
				Gaps: 0;	
QY	1	1476	1476	1476	1476
DB	1	1476	1476	1476	1476
QY	61	1476	1476	1476	1476
DB	61	1476	1476	1476	1476
QY	121	1476	1476	1476	1476
DB	121	1476	1476	1476	1476
QY	181	1476	1476	1476	1476
DB	181	1476	1476	1476	1476
QY	241	1476	1476	1476	1476
DB	241	1476	1476	1476	1476
QY	301	1476	1476	1476	1476
DB	301	1476	1476	1476	1476
QY	361	1476	1476	1476	1476
DB	361	1476	1476	1476	1476
QY	421	1476	1476	1476	1476
DB	421	1476	1476	1476	1476
QY	481	1476	1476	1476	1476
DB	481	1476	1476	1476	1476
QY	541	1476	1476	1476	1476
DB	541	1476	1476	1476	1476
QY	601	1476	1476	1476	1476
DB	601	1476	1476	1476	1476
QY	661	1476	1476	1476	1476
DB	661	1476	1476	1476	1476
QY	721	1476	1476	1476	1476
DB	721	1476	1476	1476	1476
QY	781	1476	1476	1476	1476
DB	781	1476	1476	1476	1476
QY	841	1476	1476	1476	1476
DB	841	1476	1476	1476	1476
QY	901	1476	1476	1476	1476
DB	901	1476	1476	1476	1476
QY	961	1476	1476	1476	1476
DB	961	1476	1476	1476	1476
QY	1021	1476	1476	1476	1476
DB	1021	1476	1476	1476	1476
QY	1081	1476	1476	1476	1476
DB	1081	1476	1476	1476	1476
QY	1141	1476	1476	1476	1476
DB	1141	1476	1476	1476	1476
QY	1201	1476	1476	1476	1476
DB	1201	1476	1476	1476	1476
QY	1261	1476	1476	1476	1476
DB	1261	1476	1476	1476	1476
QY	1321	1476	1476	1476	1476
DB	1321	1476	1476	1476	1476
QY	1381	1476	1476	1476	1476
DB	1381	1476	1476	1476	1476
QY	1441	1476	1476	1476	1476
DB	1441	1476	1476	1476	1476
QY	1501	1476	1476	1476	1476
DB	1501	1476	1476	1476	1476
QY	1561	1476	1476	1476	1476
DB	1561	1476	1476	1476	1476
QY	1621	1476	1476	1476	1476
DB	1621	1476	1476	1476	1476
QY	1681	1476	1476	1476	1476
DB	1681	1476	1476	1476	1476
QY	1741	1476	1476	1476	1476
DB	1741	1476	1476	1476	1476
QY	1801	1476	1476	1476	1476
DB	1801	1476	1476	1476	1476
QY	1861	1476	1476	1476	1476
DB	1861	1476	1476	1476	1476
QY	1921	1476	1476	1476	1476
DB	1921	1476	1476	1476	1476
QY	1981	1476	1476	1476	1476
DB	1981	1476	1476	1476	1476
QY	2041	1476	1476	1476	1476
DB	2041	1476	1476	1476	1476
QY	2101	1476	1476	1476	1476
DB	2101	1476	1476	1476	1476
QY	2161	1476	1476	1476	1476
DB	2161	1476	1476	1476	1476
QY	2221	1476	1476	1476	1476
DB	2221	1476	1476	1476	1476
QY	2281	1476	1476	1476	1476
DB	2281	1476	1476	1476	1476
QY	2341	1476	1476	1476	1476
DB	2341	1476	1476	1476	1476
QY	2401	1476	1476	1476	1476
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QY	2461	1476	1476	1476	1476
DB	2461	1476	1476	1476	1476
QY	2521	1476	1476	1476	1476
DB	2521	1476	1476	1476	1476
QY	2581	1476	1476	1476	1476
DB	2581	1476	1476	1476	1476
QY	2641	1476	1476	1476	1476
DB	2641	1476	1476	1476	1476
QY	2701	1476	1476	1476	1476
DB	2701	1476	1476	1476	1476
QY	2761	1476	1476	1476	1476
DB	2761	1476	1476	1476	1476
QY	2821	1476	1476	1476	1476
DB	2821	1476	1476	1476	1476
QY	2881	1476	1476	1476	1476
DB	2881	1476	1476	1476	1476
QY	2941	1476	1476	1476	1476
DB	2941	1476	1476	1476	1476
QY	3001	1476	1476	1476	1476
DB	3001	1476	1476	1476	1476
QY	3061	1476	1476	1476	1476
DB	3061	1476	1476	1476	1476
QY	3121	1476	1476	1476	1476
DB	3121	1476	1476	1476	1476
QY	3181	1476	1476	1476	1476
DB	3181	1476	1476	1476	1476
QY	3241	1476	1476	1476	1476
DB	3241	1476	1476	1476	1476
QY	3301	1476	1476	1476	1476
DB	3301	1476	1476	1476	1476
QY	3361	1476	1476	1476	1476
DB	3361	1476	1476	1476	1476
QY	3421	1476	1476	1476	1476
DB	3421	1476	1476	1476	1476
QY	3481	1476	1476	1476	1476
DB	3481	1476	1476	1476	1476
QY	3541	1476	1476	1476	1476
DB	3541	1476	1476	1476	1476
QY	3601	1476	1476	1476	1476
DB	3601	1476	1476	1476	1476
QY	3661	1476	1476	1476	1476
DB	3661	1476	1476	1476	1476
QY	3721	1476	1476	1476	1476
DB	3721	1476	1476	1476	1476
QY	3781	1476	1476	1476	1476
DB	3781	1476	1476	1476	1476
QY	3841	1476	1476	1476	1476
DB	3841	1476	1476	1476	1476
QY	3901	1476	1476	1476	1476
DB	3901	1476	1476	1476	1476
QY	3961	1476	1476	1476	1476
DB	3961	1476	1476	1476	1476
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DB	4021	1476	1476	1476	1476
QY	4081	1476	1476	1476	1476
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QY	4141	1476	1476	1476	1476
DB	4141	1476	1476	1476	1476
QY	4201	1476	1476	1476	1476
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QY	4261	1476	1476	1476	1476
DB	4261	1476	1476	1476	1476
QY	4321	1476	1476	1476	1476
DB	4321	1476	1476	1476	1476
QY	4381	1476	1476	1476	1476
DB	4381	1476	1476	1476	1476
QY	4441	1476	1476	1476	1476
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QY	4501	1476	1476	1476	1476
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QY	4681	1476	1476	1476	1476
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QY	4741	1476	1476	1476	1476
DB	4741	1476	1476	1476	1476
QY	4801	1476	1476	1476	1476
DB	4801	1476	1476	1476	1476
QY	4861	1476	1476	1476	1476
DB	4861	1476	1476	1476	1476
QY	4921	1476	1476	1476	1476
DB	4921	1476	1476	1476	1476
QY	4981	1476	1476	1476	1476
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QY	5161	1476	1476	1476	1476
DB	5161	1476	1476	1476	1476
QY	5221	1476	1476	1476	1476
DB	5221	1476	1476	1476	1476
QY	5281	1476	1476	1476	1476
DB	5281	1476	1476	1476	1476
QY	5341	1476	1476	1476	1476
DB	5341	1476	1476	1476	1476
QY	5401	1476	1476	1476	1476
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QY	5461	1476	1476	1476	1476
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QY	5521	1476	1476	1476	1476
DB	5521	1476	1476	1476	1476
QY	5581	1476	1476	1476	1476
DB	5581	1476	1476	1476	1476
QY	5641	1476	1476	1476	1476
DB	5641	1476	1476	1476	1476
QY	5701	1476	1476	1476	1476
DB	5701	1476	1476	1476	1476
QY	5761	1476	1476	1476	1476
DB	5761	1476	1476	1476	1476
QY	5821	1476	1476	1476	1476

Best local similarity	93.5%	Prod. No.	4.4e 10
Matches	1447	523333710	90
	Matches	90	Indels
			Gaps
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XX claim 4; Page 16-17; 27pp; English.
 XX The present sequence represents the nucleotide sequence of the 16S rRNA
 CC gene of strain 5877 (FERM ID-6752). This strain is a new microorganism
 CC belonging to the family Acetobacteraceae, and possibly belongs to a
 CC new genus analogous to the genus Acetobacter or the genus Gluconobacter.
 CC The specification also describes other new microorganisms belonging to
 CC the Acetobacteraceae family. The microorganism has the ability to produce
 CC xylitol of D-xylose from glucose. The microorganisms were identified
 CC by collecting osmophilic microorganisms from soil, which were then
 CC examined for the ability to produce xylitol or D-xylose from glucose.
 CC The new microorganisms may be used to industrially produce xylitol or
 CC D-xylose from glucose by fermentation. The D-xylose may be used
 CC for the production of xylitol, which is used as a sweetener in the food
 CC industry. In addition, xylitol may be used for fluid therapy in the
 CC treatment of diabetes. In addition, microorganisms of strain p528 may
 CC be used for production of ethanol.
 XX
 SO Sequence 1436 bp; 352 A; 319 C; 460 G; 305 T; 0 other;

Query Match 100.0%; Score 1436; DB 21; Length 1436;
 Best Local Similarity 100.0%; Pred. No. 0;
 Mismatch 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 ttcaggtatgatgcgaacgaatgaatgaacgtatgaatacctatccagagtgaggata 120
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 DB 121 acacaggaacgaatgactaatacagatgatacctgaggtgaaaggttttttgct 180
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 DB 181 ttgaagagagcctgcctttgatgaactatgattgaatgaaggtgacaaaggtgat 240
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 DB 361 acggaagagcagatgaggaatatttgaacatgaggaacactgacccaacatgcgc 360
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 DB 421 gttatgaggaagatgcttgcgattgataaggaacttgcctgaggaagatgatacagat 420
 QY 481 ctgaagaaagaaacccgcctgaacttgcctgcagagccgcgtgaatacgaagagggctag 480
 DB 481 ctgaagaaagaaacccgcctgaacttgcctgcagagccgcgtgaatacgaagagggctag 480
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 QY 601 ttgaagaaatgtccatgattgaagattgaatgtatataatataatgaagaaacccagttgata 660
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 DB 720 ag 720

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 DB 841 agtccagacaaatgagcag 900
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 DB 961 agcgtgaaac 960
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 DB 1200 ttatgaactgaggtac 1200
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 QY 1380 gtac 1380
 DB 1380 gtac 1380
 QY 1436 aaggtgag 1436
 DB 1436 aaggtgag 1436

RESULT 2
 AAZ45682 standard: DNA; 1439 bp.

AAZ45682;
 06 APR-2000 (first entry)

Nucleotide sequence of the 16S rRNA gene of strain p528.

16S rRNA gene; strain p528; FERM BP-6751; Acetobacteraceae; xylitol;
 D-xylose, glucose, sweetener; fluid therapy; diabetes; ethanol; ss.
 Acetobacter sp.
 EP974646-A1.
 26-JAN-2000.
 07-JUL-1999; 99BP-0113149.
 08-JUL-1998; 98JP-0194472.
 30-OCT-1998; 98JP-0310398.

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 21 Matsuoka Y., Takeuchi S., Kikuchi Y., Takeuchi N., Fukui K., Yokozeki K.,
 XX White A., and others (2001).
 XX New microorganisms useful for the production of D-xylitol from xylyl
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 23 Matsuoka Y., Takeuchi S., Kikuchi Y., Takeuchi N., Fukui K., Yokozeki K.,
 XX
 24 The present sequence represents the nucleotide sequence of the 16S rRNA
 25 gene of strain 1504 (F899 bp, 67%). This strain is a new microorganism
 26 isolated from the family Acidobacterium. The specificity of this
 27 microorganism has been demonstrated by this family. The
 28 microorganism has the ability to produce xylitol from xylose
 29 and xylose. The microorganisms were identified by their ability to
 30 grow on xylose from soil, which were then examined for the ability to
 31 produce xylitol from xylose. In addition, the new microorganisms may
 32 be used as a xylitol-producing microorganism. D-xylose isomerase by
 33 treatment. The D-xylose may be used for the production of xylitol,
 34 which is used as a sweetener in the food industry. In addition, xylitol
 35 may be used for food therapy in the treatment of diabetes. In addition,
 36 microorganisms of strain 1504 may be used for production of ethanol.
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 38 Sequence (1504 bp): (40 A), (26 G), (479 C), (200 T), (3 other).
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RESULT 3

AAF90275

10 AAF90275 standard, 18NA, 1450 bp.

XX AAF90275;

XX XX

11 22-ABG-2001 (first entry)

XX

12 Nucleotide sequence of 16S rRNA of Methylobacterium nodulans.

XX

13 16S rRNA: symbiotic bacterium; methylotrophic bacterium; root nodule;

14 nitrogen fixation; leguminous plant; pollinating; early-derived pollutant;

XX SS.

XX

15 Methylobacterium nodulans.

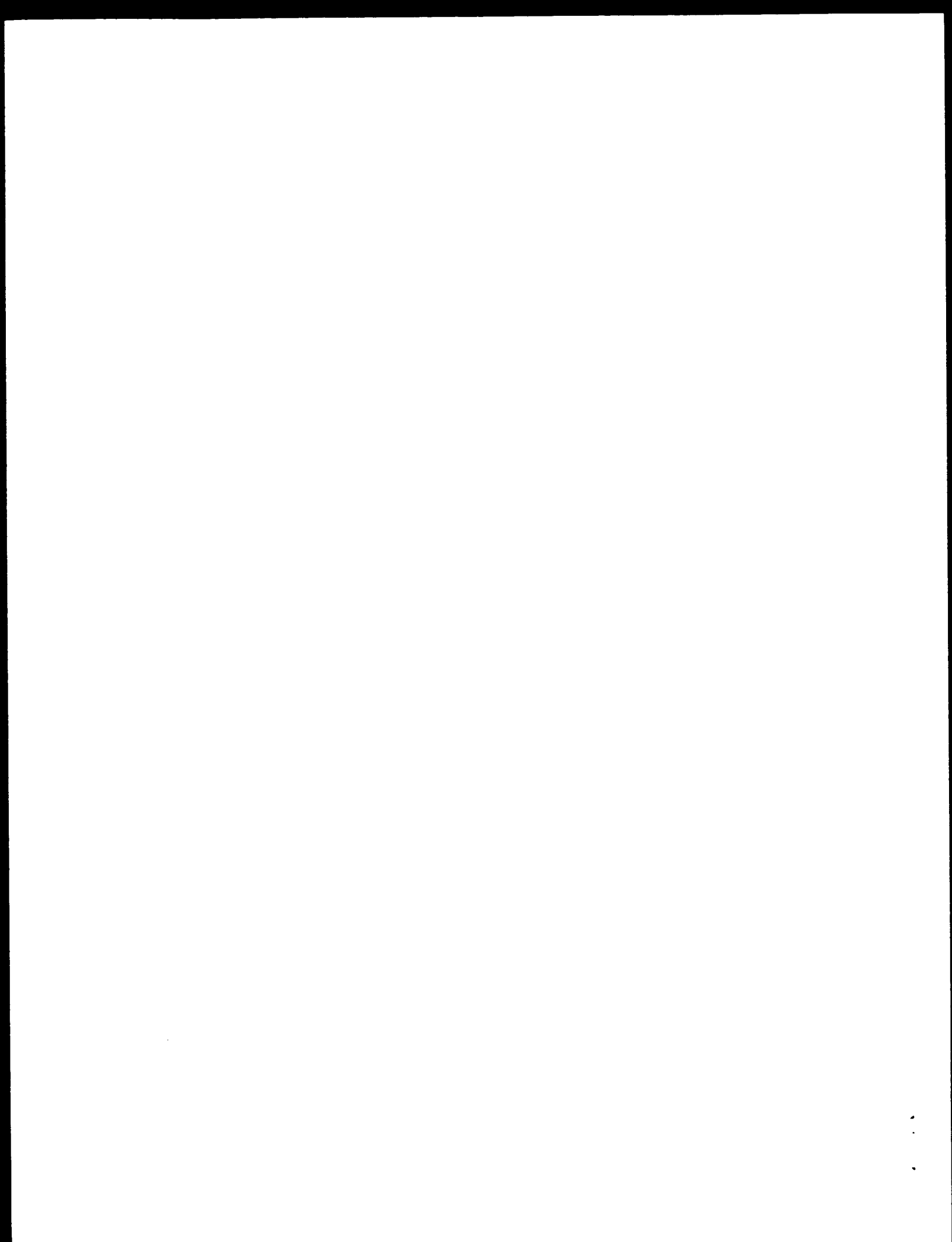
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4  ; Patent No. 5607839
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Tsubokura, Akira
7  ; APPLICANT: Yoneda, Hisashi
8  ; APPLICANT: Takaki, Mikihiro
9  ; APPLICANT: Kiyota, Takashi
10 ; TITLE OF INVENTION: BACTERIA BELONGING TO NEW GENES AND
11 ; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CARBONHIS USING SAME
12 ; NUMBER OF SEQUENCES: 1
13 ; CORRESPONDENCE ADDRESS:
14 ; ADDRESSEE: Seed & Berry
15 ; STREET: 6309 Columbia Center, 701 Fifth Avenue
16 ; CITY: Seattle
17 ; STATE: Washington
18 ; COUNTRY: USA
19 ; ZID: 98104-7092
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: Floppy disk
22 ; COMPUTER: IBM PC compatible
23 ; OPERATING SYSTEM: PC DOS/MS DOS
24 ; SOFTWARE: PatentID Release #1.0, Version #1.25
25 ; CURRENT APPLICATION DATA:
26 ; APPLICATION NUMBER: US/08/276,943
27 ; FILING DATE: 19-JUL-1994
28 ; CLASSIFICATION: 435
29 ; ATTORNEY/AGENT INFORMATION:
30 ; NAME: Makii, David J
31 ; REGISTRATION NUMBER: 31,392
32 ; REFERENCE/DOCKET NUMBER: 700085.407
33 ; TELECOMMUNICATION INFORMATION:
34 ; TELEPHONE: (206) 622-4900
35 ; TELEFAX: (206) 682-6031
36 ; TELFX: 3723836 SEEDANBERRY
37 ; INFORMATION FOR SEQ ID NO: 1:
38 ; SEQUENCE CHARACTERISTICS:
39 ; LENGTH: 1452 base pairs
40 ; TYPE: nucleic acid
41 ; STRANDEDNESS: double
42 ; TOPOLOGY: linear
43 ; MOLECULE TYPE: cDNA to rRNA
44 ; US-08-276-943-1

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: Sequence 1, Application US/089495960
: Patent No. 6040818
: GENERAL INFORMATION:
: APPLICANT: PAGI, Michel
: APPLICANT: LANDRY, Nathalie
: APPLICANT: BOUSSINOT, Maurice
: APPLICANT: HILJE, Marie-Claude
: APPLICANT: HARVEY, Mario
: APPLICANT: GAGNE, Ralfin
: TITLE OF INVENTION: BACTERIAL MASS PRODUCTION
: TITLE OF INVENTION: OF TAXANES AND FACITAXEL
: NUMBER OF SEQUENCES: 18
: CORRESPONDENT'S ADDRESS:
: ADDRESSEE: Diko, Bronstein, Roberts & Cushman, LLP
: STREET: 140 Water Street
: CITY: Boston
: STATE: MA
: COUNTRY: U.S.A.
: ZIP: 02109
: COMPUTER REAMABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/089495960
: FILING DATE: 22 DEC 1997
: CLASSIFICATION: A95
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: RESNIKOFF, David S.
: REGISTRATION NUMBER: 34,245
: REFERENCE TO PUBLICATION: 1996

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[illegible]

RESULT 12
US-08-632,470-26
; Sequence of Application US-08-632,470
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: HARTHAU, CLAUDE

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ALIGNMENTS

RESULTS

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AR042451

Locus

DEFINITION

AR042451

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

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Result No. is the number of results predicted by changes to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

us-09-902-693-4.rge

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DEFINITION	Acetobacter glaucus strain 16S ribosomal RNA, partial	05-SEP-2000

Matches 646; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

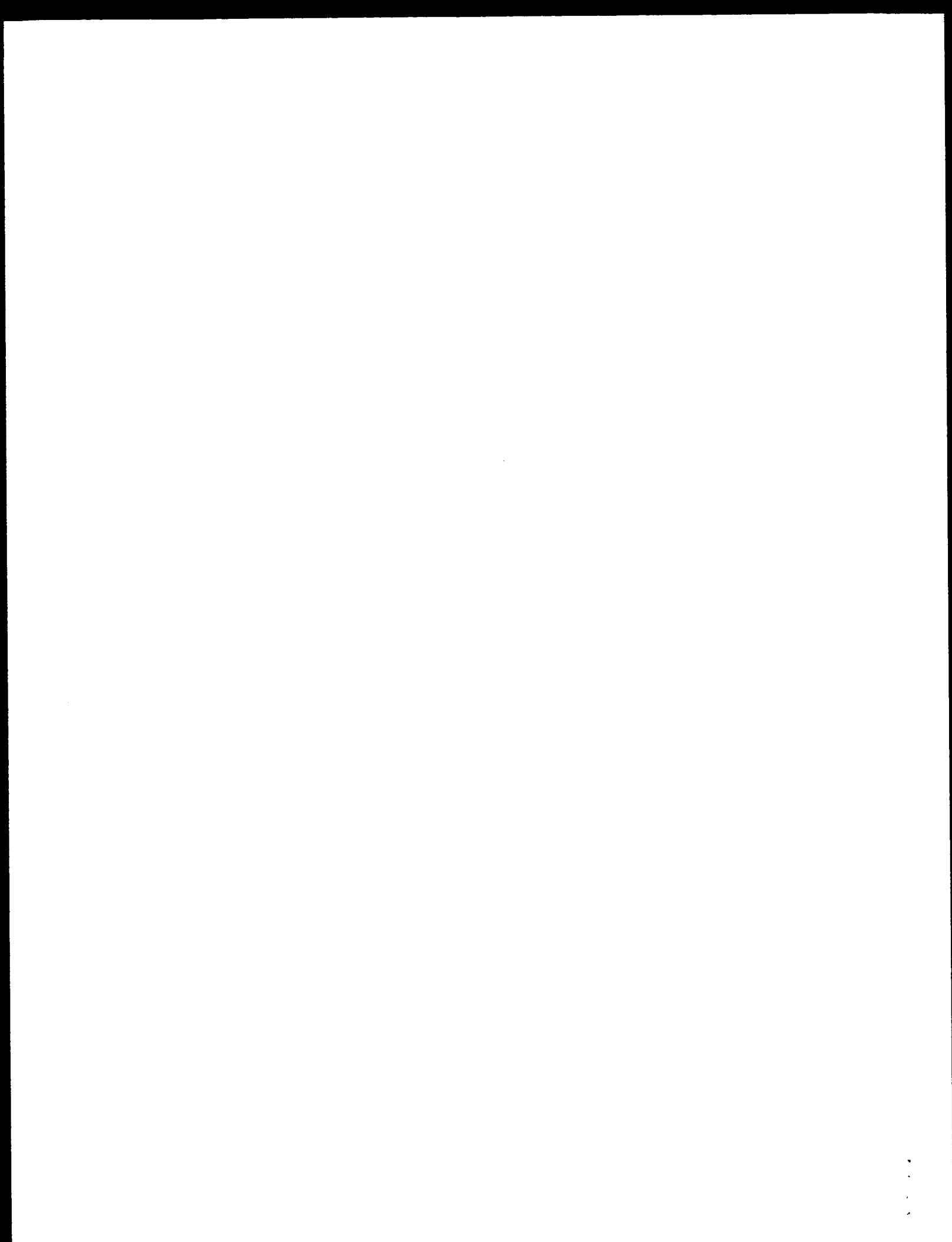
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 QY 62 tggaggt taa qqqaaacqet taa aacqet aqaacat tccaaqet qqqqataa 121
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RESULT 11
 G016S 1476 bp UNA BCT 04 NOV 1997
 DEFINITION Glucanobacter oxydans gene for 16S rRNA.
 ACCESSION X74820
 VERSION X74820.1 GI:2597906
 KEYWORDS 16S ribosomal RNA, 16S rRNA.
 SOURCE Glucanobacter oxydans.
 ORGANISM Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 Glucanobacter.
 REFERENCE 1 (bases 1 to 1476)
 AUTHORS Sievers, M.
 DIRECT SUBMISSION
 TITLE Submitted (30-JUL-1995) M. Sievers, Food Microbiology, Swiss
 FEDERAL INST. OF TECHNOLOGY, ETH, ETH Zentrum, CH-8092 Zurich,
 SWITZERLAND.
 REMARK
 REFERENCE 2 (bases 1 to 1476)
 AUTHORS Sievers, M., Ludwig, W., and Teuber, M.
 TITLE Phylogenetic positioning of Acetobacter, Glucanobacter, Rhodopila
 and Acidithiobacillus species as a branch of acidophilic bacteria in the

alpha-subclass of Proteobacteria based on 16S ribosomal DNA
 sequences
 JOURNAL Syst. Appl. Microbiol. 17, 189-196 (1994)
 REFERENCE 3 (bases 1 to 1476)
 AUTHORS Teuber, M.
 TITLE Direct Submission
 JOURNAL Submitted (03-NOV-1997) Teuber, M., Institute of Food Technology,
 Laboratory of Food Microbiology, Schweizerstrasse 9, 8092 Zurich,
 Switzerland
 COMMENT on Nov 2, 1997 this sequence version replaced gi:510845.

FEATURES
 source location/qualifiers
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 /organism "Glucanobacter oxydans"
 /strain "DSM 3503"
 /reference "Ludwig 112"
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 /product "16S ribosomal RNA"
 BASE COUNT 349 a 341 c 484 g 302 t
 ORIGIN

Query Match 88.2%; Score 609.4; DB 1; Length 1476;
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 Matches 640; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
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 QY 121 aacagagaaact qat qat aacqat qat aacqat qat aacqat tttgttgcct 180
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11 New microbes E 396 and A 361 1 useful for prodn. of all trans
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RESULT      2
US-09-902-694-4
: Sequence 4, Application US/99/02694
: GENERAL INFORMATION:
: APPLICANT: MIHARA, Yasuhiro
: APPLICANT: TAKEUCHI, Sonoko
: APPLICANT: JOJIMA, Yasuko
: APPLICANT: TENJICHI, Naoto
: APPLICANT: FUKUO, Ryo-suko
: APPLICANT: Y. K. YU, S. C.
: TITLE OF INVENTION: REVER. MICROORGANISM AND METHOD FOR PRODUCING XYLLIOL OR
: TITLE OF INVENTION: 16-XYLLIOSE
: FILE REFERENCE: 0010-1015-0
: CURRENT APPLICATION NUMBER: 09/99/02694
: PRIOR FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: 09/447,001
: PRIOR FILING DATE: 1999-07-02
: PRIOR APPLICATION NUMBER: JP 10-194472
: PRIOR FILING DATE: 1998-07-08
: PRIOR APPLICATION NUMBER: JP 10-310498
: PRIOR FILING DATE: 1998-10-30
: PRIOR APPLICATION NUMBER: JP 11-12244
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: Patent in Ver. 2.1
: SEQ ID NO 4
: LENGTH: 691
: TYPE: DNA
: ORGANISM: unknown organism
: FEATURE:
: OTHER INFORMATION: Description of Unknown organism: strain S1019
US-09-902-694-4

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RESULT      3
US-09-902-693-2
; Sequence 2, Application US/09902694
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: TAKEUCHI, Sonoko
; APPLICANT: JOJIMA, Yasuko
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: FUDOU, Fyosuke
; APPLICANT: YOROZEKI, Kenzo
; TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
; TITLE OF INVENTION: D-XYLULOSE
; FILE REFERENCE: 0010-1015-0
; CURRENT APPLICATION NUMBER: US/09/902,693
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/347,001
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: JP 10-193472
; PRIOR FILING DATE: 1998-07-08

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[illegible]

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Copyright (c) 1999-2000 Computer 343.

Maximum number of sequences in a single SW profile

February 26, 2002, 08:24:54 : Search time 4487.18 seconds
(804800 alignments)
104.79% BLASTed with update 691.

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Prod. No. is the number of results predicted by chance. To have a
score greater than or equal to the score of the result being printed,
it is derived by analysis of the total score distribution.

SUMMARIES

Seq. No.	Score	Batch	Length (bp)	Description
1	1000	64	10	BE356988 101.146_k
2	999	64	10	AW179634 SWY125600
3	998	64	10	AW179634 SWY125600
4	997	64	10	AW179634 SWY125600
5	996	64	10	AW179634 SWY125600
6	995	64	10	AW179634 SWY125600
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8	993	64	10	AW179634 SWY125600
9	992	64	10	AW179634 SWY125600
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12	989	64	10	AW179634 SWY125600
13	988	64	10	AW179634 SWY125600
14	987	64	10	AW179634 SWY125600
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23	978	64	10	AW179634 SWY125600
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34	967	64	10	AW179634 SWY125600
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14	431.6	48.0	59	10	AW179634	SWY125600
15	429.4	47.7	65	13	BE356988	101.146_k
16	428.4	47.5	721	13	CNS01008	101.146_k
17	427.7	47.3	612	11	BE356988	101.146_k
18	426.8	47.3	62	13	BE356988	101.146_k
19	425.5	47.0	55	13	AQ957271	LEPA041F
20	416.8	45.8	591	13	BE356988	101.146_k
21	416.4	45.8	591	13	BE356988	101.146_k
22	416.4	45.8	591	13	BE356988	101.146_k
23	416.4	45.8	591	13	BE356988	101.146_k
24	414.6	45.5	571	10	AW179634	SWY125600
25	414.6	45.5	602	11	BE356988	101.146_k
26	412.4	45.2	63	13	BE356988	101.146_k
27	412.2	45.2	892	13	BE356988	101.146_k
28	410.8	45.0	559	11	BE356988	101.146_k
29	409.8	44.8	577	13	BE356988	101.146_k
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31	408	44.6	553	5	AW74504	WS1333
32	406.8	44.4	520	10	AW179634	SWY125600
33	406.6	44.4	552	13	BE356988	101.146_k
34	406.6	44.4	548	13	BE356988	101.146_k
35	406.6	44.4	675	13	BE356988	101.146_k
36	406.6	44.4	741	13	BE356988	101.146_k
37	406.6	44.4	806	13	BE356988	101.146_k
38	406.2	44.3	554	5	AW74504	WS1333
39	406.2	44.3	562	11	BE356988	101.146_k
40	404.8	44.1	544	13	BE356988	101.146_k
41	404.6	44.1	687	13	BE356988	101.146_k
42	403	43.8	573	11	BE356988	101.146_k
43	402.2	43.7	550	5	AW74504	WS1333
44	299.4	43.3	561	13	BE356988	101.146_k
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ALIGNMENTS

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LOCUS	BE356988 510 bp MPEA 100.000
DEFINITION	BE356988 101.146_k MPEA 100.000
ACCESSION	BE356988
VERSION	BE356988.1
KEYWORDS	EST
SOURCE	EST
ORGANISM	Sorathum bicolor
REFERENCE	Sorathum bicolor
AUTHORS	Sorathum bicolor
TITLE	Sorathum bicolor
JOURNAL	Sorathum bicolor
COMMENT	Sorathum bicolor

Location/Qualifiers
1. 1616
/organism "Sorathum bicolor"
/db_xref "taxon:3558"


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Visser's Root 1925) nom. rev
Unpublished (1999)
2 (bases 1 to 1443)
AUTHORS Kawasaki, H. and Tashiyanti, P.
TITLE Direct Submission
JOURNAL Submitted (16-Sep-1999) to the EMBL/GenBank/
Kawasaki, The International Center for Biotechnology, Osaka
University, 2-1, Yamadaoka, Suita, Osaka 565-0871, Japan
(E-mail: kawasaki@icb.osaka-u.ac.jp, Tel: 81-6-6879-7455,
Fax: 81-6-6879-7454)
FEATURES
Location/Qualifiers
SOURCE
1..1443
/organism "Acetobacter lovaniensis"
/strain "16S 13753"
/db_xref="taxon:104100"
c1..>1443
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442 a 124 c 173 q 304 t
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Best Local Similarity 93.9%; Pred. No. 11;
Matches 649; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 1 tgaatcctcctcagagcgaacgctcagcgaatccttaccacatcgaatcagcgaacct 60
DB 8 TGATCTGGCTTCAGAGCGAAGCGCTGGCGGATAGCTTAACACATGCAAGTGGACGAACCT 67
QY 61 ttcggggttcagtcggcgagacgagcgagcagcagcagcagcagcagcagcagc 120
DB 68 TTGGGGGTTCAGTGGCGAGACGAGCGAGTACGAGCGGAGTGTGCGACGGCTGGCGGATA 127
QY 121 acacacacacacacacacacacacacacacacacacacacacacacacacacac 180
DB 128 ACTCTGGAAACTGGAGCTTAATAGCGCATGATAGCTGAGGGCTTAAGGGCGCAAGTGGCT 187
QY 181 ttcggggttcagtcggcgagacgagcagcagcagcagcagcagcagcagcagc 240
DB 188 GTGGAGAGAGCTGGCTTCGATAGCTAGTTCGTCGGGCTTAAGGGCTACGACGAGCGATGAT 247
QY 241 caatcctcctcagagcgaacgctcagcgaatccttaccacatcgaatcagcgaac 300
DB 248 CGATAGCTGGCTTCAGAGCGAAGCGCTGGCGGATAGCTTAACACATGCAAGTGGACGAACCT 307
QY 301 acgagagcgaacgctcagcgaatccttaccacatcgaatcagcgaacgctcagc 360
DB 308 ACGGAGCGCAGCAGTCTGGGATTTGAGCAATGCGGCGCAACCTGATCCAGCAATGCGCG 367
QY 361 gtagatcagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 420
DB 368 GTGGTGAAGAGCTCTTCGATTTGAAAGCAGCTTTTCGAGAGGGGACGATGATGACGGTAC 427
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DB 488 CGTCTCTCGAATGAGTGGGCTTAAGAGCGGCTGAGTGGGCTTACAGAGTGAATGAGAA 547
QY 541 atcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
DB 548 APTCTGGGCTTAACCTGGGCTGAGTTCGATAGCTGAGAGTACGATGAGAGAGAGG 607
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QY 661 aagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 691

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db 668 AGGCGGACACCTGGCTCAGTCACTGACTGACGCTGA 698

RESULT 2
APRVA 1479 bp DNA 1901 05 Nov 1997
DEFINITION A-pasteurianus gene for 16S ribosomal RNA.
ACCESSION X71863.1 GI:2507822
VERSION 16S ribosomal RNA; 16S rRNA.
KEYWORDS Acetobacter pasteurianus.
SOURCE Acetobacter pasteurianus.
ORGANISM Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Acetobacter.
REFERENCE
1 (bases 1 to 1479)
Sievers, M., Ludwig, W. and Teuber, M.
Phylogenetic positioning of Acetobacter, Gluconobacter, Rhodospirillum
and Acidiphilium species as a branch of acidophilic bacteria in the
alpha-subclass of Proteobacteria based on 16S ribosomal DNA
sequences
Syst. Appl. Microbiol. 17, 189-196 (1994)
2 (bases 1 to 1479)
Sievers, M.
Direct Submission
Submitted (07-MAY-1994) M. Sievers, Swiss Federal Inst of
Technology ETH, Food Microbiology, ETH-Zentrum, LF9, 8092 Zurich,
SWITZERLAND
REMARK
3 (bases 1 to 1479)
Teuber, M.
Direct Submission
Submitted (04-NOV-1997) Teuber, M., Institute of Food Technology,
Laboratory of Food Microbiology, Schmelzbergstrasse 9, 8092 Zurich,
Switzerland
COMMENT
On Nov 8, 1997 this sequence version replaced GI:472865.
FEATURES
Location/Qualifiers
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1..1479
/organism "Acetobacter pasteurianus"
/isolate "185 22.1"
/db_xref="taxon:438"
c1..>1479
/product "16S ribosomal RNA"
BASE COUNT 350 a 333 c 486 g 310 t
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Best Local Similarity 93.5%; Pred. No. 12;
Matches 646; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 tgaatcctcctcagagcgaacgctcagcgaatccttaccacatcgaatcagcgaac 60
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QY 61 ttcggggttcagtcggcgagacgagcgagcagcagcagcagcagcagcagcagc 120
DB 66 TTGGGGGTTCAGTGGCGAGACGAGCGAGTACGAGCGGAGTGTGCGACGGCTGGCGGATA 125
QY 121 acacacacacacacacacacacacacacacacacacacacacacacacacacac 180
DB 126 ACTCTGGAAACTGGAGCTTAATAGCGCATGATAGCTGAGGGCTTAAGGGCGCAAGTGGCT 185
QY 181 ttcggggttcagtcggcgagacgagcgagcagcagcagcagcagcagcagcagc 240
DB 186 GTGGAGAGAGCTGGCTTCGATAGCTAGTTCGTCGGGCTTAAGGGCTACGACGAGCGATGAT 245
QY 241 caatcctcctcagagcgaacgctcagcgaatccttaccacatcgaatcagcgaac 300
DB 246 CAATAGCTGGCTTCAGAGCGAAGCGCTGGCGGATAGCTTAACACATGCAAGTGGACGAACCT 305
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Fax: 81-6-6879-7454)

FEATURES	Location/Qualifiers
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source
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rRNA

gene
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100%	100%	100%	100%	100%	100%

DEFINITION

ACCESSION
NUMBER
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VERSION AlO32349.1 01:9971302

KEYWORDS: 16S ribosomal RNA, 16S rRNA.

SOURCE: Acetobacter (stunensis (strain: FC 13751) DNA.

ORGANISM: *Acetobacter (C) tennensis*

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E-mail: mahdian@uic.edu

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Yamada, Y., Seki, T., Ichimura, Y. and
Kawasaki, P., Kawasaki, H.

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TABLE: Taxonomic study of the genus *Acetobacter* with descriptions of

Accumbacter tuberosus sp. nov., *Accubacter propolis* sp.

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visser 't Hooft 1925) nom. rev

JOURNAL, Unpublished (1999)

REFERENCE 2 (bases 1 to 1446)

Authors: Kawasaki, I., and Puspita, L.

1. Introduction

Kawasaki, The International Center for Biotechnology, Osaka

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2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 
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[illegible]

[illegible]

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-29

Query Match 63.6% Score 439.4 DB 2 Length 1440
Best Local Similarity 79.0% Pred. No. 1.7e-132
Matches 554 Conservative 0 Mismatches 141 Indels 16 Gaps 23

QY 5 cct qct cag aag aag aag cgt qgc qgc aat qct taa caca cta cca aat cgc aac cct ttc q 64
DB 1 cct ggc tca gaa gaa gaa ggt taa cgt tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc 60
QY 65 qg ----- qtt aat qgc qgc aag cgt qat aac cgt aag aac cct at cct qat 110
DB 61 ggc ctt ggc tgc cca gtt tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc 120
QY 111 qtc qgc aat aac aat aac aat qat aat aac cca aat aat aac cct aac aac cct 170
DB 121 gta gca aat aac ctt tgc aaaa taaa aac taa tgc tgc tgc tgc tgc tgc tgc tgc 178
QY 171 ttt qtc qgc tgc aag aag aag cgt qgc ttt qat tgc tgc tgc tgc tgc tgc tgc tgc 240
DB 179 ttt tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc 248
QY 231 aag cga tgc aat aat aat qat tgc aag aat qat cgc aac aat qat aac aac cgt 290
DB 239 aag cga tgc aat aat aat qat tgc aag aat qat cgc aac aat qat aac aac cgt 298
QY 291 cgc aat cgc aag aag aag aag cgt qgc aat tgc aac aat aac aac aac cct qat cca 350
DB 299 cgc aat cgc aag aag aag aag cgt qgc aat tgc aac aat aac aac aac cct qat cca 358
QY 351 qca at cgc cgt qat qat aag aag aat ctc qgc ttt aaaa cca cct tgc aag aat q 410
DB 359 gca at cgc aag tgc aag tgc aag tgc aag tgc aag tgc aag tgc aag tgc aag tgc 418
QY 411 atg aag tgc aat aat aat aat aat aat aat aat aat aat aat aat aat aat aat 470
DB 419 atg aag tgc aat aat aat aat aat aat aat aat aat aat aat aat aat aat aat 478
QY 471 aag cgc tgc aat qat cgc aat aat qgc aat aag aag aag cgt aag cgt ttt at aat 530
DB 479 aag cgc tgc aat qat cgc aat aat qgc aat aag aag aag cgt aag cgt ttt at aat 538
QY 531 cgc aat qat aat cgc aag aag aag aag aag aag aag aag aag aag aag aag aag 590
DB 539 tgc aag tgc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 598
QY 591 cgc aag aag aat tgc aag aat cgc aat aat qgc aat aat qgc aat aat qgc aat 650
DB 599 tag tgc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 658
QY 651 cgc aat tgc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 699

QY 111 atg aag aat aac aat qgc aat aat aac aat qat aat aac aat qat aat aac aat qat 170
DB 121 gta gca aat aac ctt tgc aaaa taaa aac taa tgc tgc tgc tgc tgc tgc tgc tgc 178
QY 171 ttt qtc qgc tgc aag aag aag cgt qgc ttt qat tgc tgc tgc tgc tgc tgc tgc tgc 230
DB 179 ttt tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc tgc 238
QY 231 aag cga tgc aat aat aat qat tgc aag aat qat cgc aac aat qat aac aac cgt 290
DB 239 aag cga tgc aat aat aat qat tgc aag aat qat cgc aac aat qat aac aac cgt 298
QY 291 cgc aat cgc aag aag aag aag cgt qgc aat tgc aac aat aac aac aac cct qat cca 350
DB 299 cgc aat cgc aag aag aag aag cgt qgc aat tgc aac aat aac aac aac cct qat cca 358
QY 351 qca at cgc cgt qat qat aag aag aat ctc qgc ttt aaaa cca cct tgc aag aat q 410
DB 359 gca at cgc aag tgc aag tgc aag tgc aag tgc aag tgc aag tgc aag tgc aag tgc 418
QY 411 atg aag tgc aat aat aat aat aat aat aat aat aat aat aat aat aat aat aat 470
DB 419 atg aag tgc aat aat aat aat aat aat aat aat aat aat aat aat aat aat aat 478
QY 471 aag cgc tgc aat qat cgc aat aat qgc aat aag aag aag cgt aag cgt ttt at aat 530
DB 479 aag cgc tgc aat qat cgc aat aat qgc aat aag aag aag cgt aag cgt ttt at aat 538
QY 531 cgc aat qat aat cgc aag aag aag aag aag aag aag aag aag aag aag aag aag 590
DB 539 tgc aag tgc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 598
QY 591 cgc aag aag aat tgc aag aat cgc aat aat qgc aat aat qgc aat aat qgc aat 650
DB 599 tag tgc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 658
QY 651 cgc aat tgc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 699

RESULT 14
US-08-632-470-29
Sequence 29, Application US/986,324/70
Patent No. 5,976,791
GENERAL INFORMATION:
APPLICANT: MARILLAT, CLAUDE
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
HYBRIDIZING SPECIFICALLY TO RIBONUCLEIC ACID
TITLE OF INVENTION: THEIR USE AS PROBES OF PRIMER
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVE & BERTRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
COMPUTER TYPE: EASY-4-86
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICANT: MARILLAT, CLAUDE
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERTRIDGE, WILLIAM P.
REGISTRATION NUMBER: 35,024
RETURNED/NOTED NUMBER: WHP 35248

